CLAIMS

We claim:

1. A method of analyzing micro-satellite loci, comprising steps of:

a) providing primers for co-amplifying a set of at least three microsatellite loci of genomic DNA, comprising at least one mono-nucleotide repeat locus and at least two tetra-nucleotide repeat loci;

b) co-amplifying the set of at least three microsatellite loci from at least one sample of genomic DNA in a multiplex amplification reaction, using the primers, thereby producing amplified DNA fragments; and

c) determining the size of the amplified DNA fragments.

2. The method of claim 1, wherein the genomic DNA is human genomic DNA.

3. The method of claim 2, wherein the at least two tetra-nucleotide repeat loci are selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

4. The method of claim 2, wherein the at least one mono-nucleotide repeat locus is selected from the group consisting of BAT-25, BAT-26, MONO-11, and MONO-15.

5. The method of claim 2, wherein the set of at least three microsatellite loci is a set of at least five microsatellite loci, comprising:

at least two mono-nucleotide repeat loci selected from the group consisting of BAT-25, BAT-26, MONO-11, and MONO-15; and

at least three tetra-nucleotide repeat loci selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

6. The method of claim 2, wherein at least one of the primers provided in step (a) has a nucleic acid sequence selected from the group of primer sequences identified by: SEQ ID NO: 1- 62.

7. The method of claim 2, wherein the set of at least three microsatellite loci is a set of at least nine microsatellite loci, comprising BAT-25, BAT-26, MONO-15, D1S518, D3S2432, D7S1808, D7S3070, D7S3046, D10S1426.

8. The method of claim 7, wherein the set of at least nine microsatellite loci is co-amplified using at least one primer for each locus selected from the group consisting of:

SEQ ID NO: 1 and SEQ ID NO: 60 when the locus is BAT-25,
SEQ ID NO: 61 and SEQ ID NO: 62 when the locus is BAT-26,
SEQ ID NO: 7 and SEQ ID NO: 8 when the locus is MONO-15,
SEQ ID NO: 49 and SEQ ID NO: 50 when the locus is D1S518,
SEQ ID NO: 17 and SEQ ID NO: 59 when the locus is D3S2432,
SEQ ID NO: 51 and SEQ ID NO: 52 when the locus is D7S1808,
SEQ ID NO: 53 and SEQ ID NO: 54 when the locus is D7S3070,
SEQ ID NO: 55 and SEQ ID NO: 56 when the locus is D7S3046, and
SEQ ID NO: 57 and SEQ ID NO: 58 when the locus is D10S1426.

9. The method of claim 1, wherein the set of at least three microsatellite loci is co-amplified in step (c) using at least one oligonucleotide primer for each locus which is fluorescently labeled.

10. The method of claim 1, wherein the at least one sample of genomic DNA comprises a first sample of genomic DNA originating from normal non-cancerous biological material from an individual and a second sample of genomic DNA originating from a tumor of the individual, the method further comprising:

detecting microsatellite instability by comparing the size of the amplified DNA fragments produced from co-amplifying the first sample of genomic DNA to the size of the amplified DNA fragments produced from co-amplifying the second sample of genomic DNA.

11. The method of claim 10, wherein the microsatellite instability results are used in prognostic tumor diagnosis.

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12. The method of claim 10, wherein the microsatellite instability results are used in the diagnosis of familial tumor predisposition.

13. The method of claim 10, wherein the microsatellite instability results are used to detect cancerous tumors of the gastro-intestinal system and of the endometrium.

14. The method of claim 13 wherein the cancerous tumors are tumors from a colorectal cancer.

15. A method of detecting microsatellite instability in genomic DNA, comprising the steps of:

a) providing primers for co-amplifying a set of at least three microsatellite loci of genomic DNA, comprising at least one mono-nucleotide repeat locus and at least two tetra-nucleotide repeat loci;

b) co-amplifying the set of at least three microsatellite loci from a first sample of genomic DNA originating from normal non-cancerous biological material from an individual and a from a second sample of genomic DNA originating from a second biological material from the individual, in separate multiplex amplification reactions, using the primers, thereby producing first amplified DNA fragments from the first sample and second amplified DNA fragments from the second sample; and

c) comparing the size of first amplified DNA fragments to the size of the second amplified DNA fragments to detect instability in any of the at least three microsatellite loci of the second genomic DNA.

16. The method of claim 15, wherein the primers provided in step (a) are primers to microsatellite loci of human genomic DNA.

17. The method of claim 16, wherein the two tetra-nucleotide repeat loci are selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

18. The method of claim 16, wherein the mono-nucleotide repeat locus is selected from the group consisting of BAT-25, BAT-26, MONO-11, and MONO-15.

19. The method of claim 16, wherein the set of at least three microsatellite loci is a set of at least five microsatellite loci, comprising two mono-nucleotide repeat loci selected from the group consisting of BAT-25, BAT-26, MONO-11, and MONO-15, and three tetra-nucleotide repeat loci selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

20. The method of claim 16, wherein at least one of the primers provided in step (a) has a nucleic acid sequence selected from the group of primer sequences identified by: SEQ ID NO: 1- 62.

21. The method of claim 15, wherein the at least one primer for each locus provided in step (a) is fluorescently labeled.

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22. The method of claim 16, wherein the set of at least two microsatellite loci is a set of at least nine microsatellite loci, comprising: BAT-25, BAT-26, MONO-15, D1S518, D3S2432, D7S1808, D7S3070, D7S3046, D10S1426.

23. The method of claim 22, wherein the set of at least nine microsatellite loci is co-amplified using at least one primer for each locus selected from the group consisting of:

SEQ ID NO: 1 and SEQ ID NO: 60 when the locus is BAT-25,

SEQ ID NO: 61 and SEQ ID NO: 62 when the locus is BAT-26,

SEQ ID NO: 7 and SEQ ID NO: 8 when the locus is MONO-15,

SEQ ID NO: 47 and SEQ ID NO: 50 when the locus is [redacted]S518,
SEQ ID NO: 17 and SEQ ID NO: 59 when the locus is D3S2432,
SEQ ID NO: 51 and SEQ ID NO: 52 when the locus is D7S1808,
SEQ ID NO: 53 and SEQ ID NO: 54 when the locus is D7S3070,
SEQ ID NO: 55 and SEQ ID NO: 56 when the locus is D7S3046, and
SEQ ID NO: 57 and SEQ ID NO: 58 when the locus is D10S1426.

24. The method of claim 15, wherein the second sample of biological material is selected from the group consisting of: tumor tissue, disseminated cells, feces, blood cells, blood plasma, serum, lymph nodes, urine, and other bodily fluids.

25. The method of claim 15, wherein the microsatellite instability results are used in prognostic tumor diagnosis.

26. The method of claim 15, wherein the microsatellite instability results are used in the diagnosis of familial tumor predisposition.

27. The method of claim 15, wherein the microsatellite instability results are used to detect cancerous tumors of the gastro-intestinal system and of the endometrium.

28. The method of claim 27 wherein the cancerous tumors are tumors from a colorectal cancer.

29. A method of analyzing at least one mono-nucleotide repeat locus, comprising the steps of:

a) providing at least one primer for at least one mono-nucleotide repeat locus of human genomic DNA selected from the group consisting of MONO-11 and MONO-15;

b) amplifying at least one mono-nucleotide repeat locus from a sample of genomic DNA originating from a biological material from an individual, using the at least one primer, thereby producing amplified DNA fragments; and

c) determining the size of the amplified DNA fragments.

30. The method of claim 29, wherein the at least one mono-nucleotide repeat locus is co-amplified using at least one primer selected from the group consisting of: SEQ ID NO: 5-8.

31. The method of claim 29, wherein the at least one mono-nucleotide repeat locus is amplified using at least one oligonucleotide primer which is fluorescently labeled.

32. The method of claim 29, wherein the biological material is selected from the group consisting of: tumor tissue, disseminated cells, feces, blood cells, blood plasma, serum, lymph nodes, urine, and other bodily fluids.

33. The method of claim 29, further comprising detecting microsatellite instability at the at least one mono-nucleotide repeat locus by comparing the size of the amplified DNA fragments to the most commonly observed allele size at that locus in a human population.

34. The method of claim 29, further comprising amplifying the at least one mono-nucleotide repeat locus of a sample of human genomic DNA from normal non-cancerous biological material from the individual, and comparing resulting second amplified DNA fragments to the amplified DNA fragments obtained in step (b) to detect microsatellite instability in step (c).

35. A kit for analyzing microsatellite loci of human genomic DNA, comprising:

a single container with oligonucleotide primers for co-amplifying a set of at least three microsatellite loci of human genomic DNA, the set comprising one mono-nucleotide repeat locus and two tetra-nucleotide repeat loci.

36. The kit of claim 35, wherein the two tetra-nucleotide repeat loci are selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

37. The kit of claim 35, wherein the mono-nucleotide repeat locus is selected from the group consisting of BAT-25, BAT-26, MONO-11, and MONO-15.

38. The kit of claim 35, wherein the set of at least three microsatellite loci is a set of at least five microsatellite loci, comprising two mono-nucleotide repeat loci selected from the group consisting of BAT-25, BAT-26, MONO-11, and MONO-15, and three tetra-nucleotide repeat loci selected from the group consisting of FGA, D1S518, D1S547, D1S1677, D2S1790, D3S2432, D5S818, D5S2849, D6S1053, D7S3046, D7S1808, D7S3070, D8S1179, D9S2169, D10S1426, D10S2470, D12S391, D17S1294, D17S1299, and D18S51.

39. The kit of claim 35, wherein the set of at least two microsatellite loci is a set of at least nine microsatellite loci, comprising: BAT-25, BAT-26, MONO-15, D1S518, D3S2432, D7S1808, D7S3070, D7S3046, D10S1426.

40. The kit of claim 35, wherein at least one of the oligonucleotide primers is selected from the group consisting of:

SEQ ID NO: 1 and SEQ ID NO: 60 when the locus is BAT-25,
SEQ ID NO: 61 and SEQ ID NO: 62 when the locus is BAT-26,
SEQ ID NO: 7 and SEQ ID NO: 8 when the locus is MONO-15,
SEQ ID NO: 49 and SEQ ID NO: 50 when the locus is D1S518,
SEQ ID NO: 17 and SEQ ID NO: 59 when the locus is D3S2432,
SEQ ID NO: 51 and SEQ ID NO: 52 when the locus is D7S1808,
SEQ ID NO: 53 and SEQ ID NO: 54 when the locus is D7S3070,
SEQ ID NO: 55 and SEQ ID NO: 56 when the locus is D7S3046, and
SEQ ID NO: 57 and SEQ ID NO: 58 when the locus is D10S1426.

41. The kit of claim 35, wherein at least one oligonucleotide primer for each of the at least three microsatellite loci in the set is fluorescently labeled.

42. The kit of claim 35, wherein the kit further comprises a thermostable polymerase.

43. The kit of claim 35, wherein the kit further comprises first control DNA isolated from normal non-cancerous biological material, and second control DNA from biological material lacking mismatch repair genes.

44. The kit of claim 35, wherein instability in the set of microsatellite loci co-amplified by the primers can be used in prognostic tumor diagnosis.

45. The kit of claim 35, wherein instability in the set of microsatellite loci co-amplified by the primers can be used in the diagnosis of familial tumor predisposition.

46. The kit of claim 35, wherein instability in the set of microsatellite loci co-amplified by the primers is an indication of tumors of the gastrointestinal system or of the endometrium.

47. The kit of claim 44, wherein the microsatellite instability is an indication of colorectal cancer.

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